

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Wang, Elizabeth A.
Rosen, Vicki A.
Wozney, John M.
- (ii) TITLE OF INVENTION: Novel BMP Products
- (iii) NUMBER OF SEQUENCES: 6
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: LEGAL AFFAIRS, GENETICS INSTITUTE, INC.
(B) STREET: 87 CAMBRIDGEPARK DRIVE
(C) CITY: CAMBRIDGE
(D) STATE: MA
(E) COUNTRY: USA
(F) ZIP: 02140
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US
(B) FILING DATE:
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: KAPINOS, ELLEN J.
(B) REGISTRATION NUMBER: 32,245
(C) REFERENCE/DOCKET NUMBER: GI5160C
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 617-876-1170
(B) TELEFAX: 617-876-5851

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 592 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: BOS TAURUS
- (vii) IMMEDIATE SOURCE:

T060E0329060

(A) LIBRARY: VINE GENOMIC IN LAMBDA JI
(B) CLONE: LAMBDA BP-21

(viii) POSITION IN GENOME:
(C) UNITS: bp

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..390

(ix) FEATURE:
(A) NAME/KEY: mat_peptide
(B) LOCATION: 46..387

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
GGC CAC GAT GGG AAA GGA CAC CCT CTC CAC AGA AGA GAA AAG CGG CAA      48
Gly His Asp Gly Lys Gly His Pro Leu His Arg Arg Glu Lys Arg Gln
-15                               -10                               -5                               1

GCA AAA CAC AAA CAG CGG AAA CGC CTC AAG TCC AGC TGT AAG AGA CAC      96
Ala Lys His Lys Gln Arg Lys Arg Leu Lys Ser Ser Cys Lys Arg His
                               5                               10                               15

CCT TTA TAT GTG GAC TTC AGT GAT GTG GGG TGG AAT GAC TGG ATC GTT     144
Pro Leu Tyr Val Asp Phe Ser Asp Val Gly Trp Asn Asp Trp Ile Val
                               20                               25                               30

GCA CCG CCG GGG TAT CAT GCC TTT TAC TGC CAT GGG GAG TGC CCT TTT     192
Ala Pro Pro Gly Tyr His Ala Phe Tyr Cys His Gly Glu Cys Pro Phe
                               35                               40                               45

CCC CTG GCC GAT CAC CTT AAC TCC ACG AAT CAT GCC ATT CTC CAA ACT     240
Pro Leu Ala Asp His Leu Asn Ser Thr Asn His Ala Ile Leu Gln Thr
50                               55                               60                               65

CTG GTC AAC TCA GTT AAC TCT AAG ATT CCC AAG GCA TGC TGT GTC CCA     288
Leu Val Asn Ser Val Asn Ser Lys Ile Pro Lys Ala Cys Cys Val Pro
                               70                               75                               80

ACA GAG CTC AGC GCC ATC TCC ATG CTG TAC CTT GAT GAG AAT GAG AAG     336
Thr Glu Leu Ser Ala Ile Ser Met Leu Tyr Leu Asp Glu Asn Glu Lys
                               85                               90                               95

GTG GTA TTA AAG AAC TAT CAG GAC ATG GTT GTC GAG GGT TGT GGG TGT     384
Val Val Leu Lys Asn Tyr Gln Asp Met Val Val Glu Gly Cys Gly Cys
100                               105                               110

CGT TAGCACAGCA AAATAAAATA TAAATATATA TATATATATA TTAGAAAAAC      437
Arg
115

AGCAAAAAAA TCAAGTTGAC ACTTTAATAT TTCCAATGA AGACTTTATT TATGGAATGG     497

AATGGAGAAA AAGAAAAACA CAGCTATTTT GAAACTATA TTTATATCTA CCGAAAAGAA     557

GTTGGGAAAA CAAATATTTT AATCAGAGAA TTATT                                592
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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Gly His Asp Gly Lys Gly His Pro Leu His Arg Arg Glu Lys Arg Gln
-15 -10 -5 1

Ala Lys His Lys Gln Arg Lys Arg Leu Lys Ser Ser Cys Lys Arg His
5 10 15

Pro Leu Tyr Val Asp Phe Ser Asp Val Gly Trp Asn Asp Trp Ile Val
20 25 30

Ala Pro Pro Gly Tyr His Ala Phe Tyr Cys His Gly Glu Cys Pro Phe
35 40 45

Pro Leu Ala Asp His Leu Asn Ser Thr Asn His Ala Ile Leu Gln Thr
50 55 60 65

Leu Val Asn Ser Val Asn Ser Lys Ile Pro Lys Ala Cys Cys Val Pro
70 75 80

Thr Glu Leu Ser Ala Ile Ser Met Leu Tyr Leu Asp Glu Asn Glu Lys
85 90 95

Val Val Leu Lys Asn Tyr Gln Asp Met Val Val Glu Gly Cys Gly Cys
100 105 110

Arg

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1607 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (G) CELL TYPE: Osteosarcoma Cell Line
- (H) CELL LINE: U-20S

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: U20S cDNA in Lambda GT10

(B) CLONE: ~~1~~oda U20S-39

(viii) POSITION IN GENOME:

(C) UNITS: bp

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 356..1546

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 1202..1543

(ix) FEATURE:

(A) NAME/KEY: mRNA

(B) LOCATION: 14..1607

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: 356..424

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GTGACTCTA GAGTGTGTGT CAGCACTTGG CTGGGGACTT CTTGAACTTG CAGGGAGAAT 60
AACTTGCGCA CCCCACTTTG CGCCGGTGCC TTTGCCCCAG CGGAGCCTGC TTCGCCATCT 120
CGGAGCCCCA CCGCCCCTCC ACTCCTCGGC CTTGCCCGAC ACTGAGACGC TGTTCCCAGC 180
GTGAAAAGAG AGACTGCGCG GCCGGCACCC GGGAGAAGGA GGAGGCAAAG AAAAGGAACG 240
GACATTCGGT CTTGCGCCA GGTCTTTGA CCAGAGTTTT TCCATGTGGA CGCTCTTTCA 300
ATGGACGTGT CCCCgcGTGC TTCTTAGACG GACTGCGGTC TCCTAAAGGT CGACC ATG 358
Met
-282
GTG GCC GGG ACC CGC TGT CTT CTA GCG TTG CTG CTT CCC CAG GTC CTC 406
Val Ala Gly Thr Arg Cys Leu Leu Ala Leu Leu Leu Pro Gln Val Leu
-280 -275 -270
CTG GGC GGC GCG GCT GGC CTC GTT CCG GAG CTG GGC CGC AGG AAG TTC 454
Leu Gly Gly Ala Ala Gly Leu Val Pro Glu Leu Gly Arg Arg Lys Phe
-265 -260 -255 -250
GCG GCG GCG TCG TCG GGC CGC CCC TCA TCC CAG CCC TCT GAC GAG GTC 502
Ala Ala Ala Ser Ser Gly Arg Pro Ser Ser Gln Pro Ser Asp Glu Val
-245 -240 -235
CTG AGC GAG TTC GAG TTG CGG CTG CTC AGC ATG TTC GGC CTG AAA CAG 550
Leu Ser Glu Phe Glu Leu Arg Leu Leu Ser Met Phe Gly Leu Lys Gln
-230 -225 -220
AGA CCC ACC CCC AGC AGG GAC GCC GTG GTG CCC CCC TAC ATG CTA GAC 598
Arg Pro Thr Pro Ser Arg Asp Ala Val Val Pro Pro Tyr Met Leu Asp
-215 -210 -205
CTG TAT CGC AGG CAC TCA GGT CAG CCG GGC TCA CCC GCC CCA GAC CAC 646

Leu	Tyr	Arg	Arg	His	Ser	Gly	Gln	Pro	Gly	Ser	Pro	Ala	Pro	Asp	His	
-200						-195					-190					
CGG	TTG	GAG	AGG	GCA	GCC	AGC	CGA	GCC	AAC	ACT	GTG	CGC	AGC	TTC	CAC	694
Arg	Leu	Glu	Arg	Ala	Ala	Ser	Arg	Ala	Asn	Thr	Val	Arg	Ser	Phe	His	
-185					-180					-175					-170	
CAT	GAA	GAA	TCT	TTG	GAA	GAA	CTA	CCA	GAA	ACG	AGT	GGG	AAA	ACA	ACC	742
His	Glu	Glu	Ser	Leu	Glu	Glu	Leu	Pro	Glu	Thr	Ser	Gly	Lys	Thr	Thr	
				-165					-160					-155		
CGG	AGA	TTC	TTC	TTT	AAT	TTA	AGT	TCT	ATC	CCC	ACG	GAG	GAG	TTT	ATC	790
Arg	Arg	Phe	Phe	Phe	Asn	Leu	Ser	Ser	Ile	Pro	Thr	Glu	Glu	Phe	Ile	
			-150					-145					-140			
ACC	TCA	GCA	GAG	CTT	CAG	GTT	TTC	CGA	GAA	CAG	ATG	CAA	GAT	GCT	TTA	838
Thr	Ser	Ala	Glu	Leu	Gln	Val	Phe	Arg	Glu	Gln	Met	Gln	Asp	Ala	Leu	
		-135					-130					-125				
CGA	AAC	AAT	AGC	AGT	TTC	CAT	CAC	CGA	ATT	AAT	ATT	TAT	GAA	ATC	ATA	886
Gly	Asn	Asn	Ser	Ser	Phe	His	His	Arg	Ile	Asn	Ile	Tyr	Glu	Ile	Ile	
	-120					-115					-110					
AAA	CCT	GCA	ACA	GCC	AAC	TCG	AAA	TTC	CCC	GTG	ACC	AGA	CTT	TTG	GAC	934
Lys	Pro	Ala	Thr	Ala	Asn	Ser	Lys	Phe	Pro	Val	Thr	Arg	Leu	Leu	Asp	
-105					-100					-95					-90	
ACC	AGG	TTG	GTG	AAT	CAG	AAT	GCA	AGC	AGG	TGG	GAA	AGT	TTT	GAT	GTC	982
Thr	Arg	Leu	Val	Asn	Gln	Asn	Ala	Ser	Arg	Trp	Glu	Ser	Phe	Asp	Val	
				-85					-80					-75		
ACC	CCC	GCT	GTG	ATG	CGG	TGG	ACT	GCA	CAG	GGA	CAC	GCC	AAC	CAT	GGA	1030
Thr	Pro	Ala	Val	Met	Arg	Trp	Thr	Ala	Gln	Gly	His	Ala	Asn	His	Gly	
			-70					-65				-60				
TTG	GTG	GTG	GAA	GTG	GCC	CAC	TTG	GAG	GAG	AAA	CAA	GGT	GTC	TCC	AAG	1078
Phe	Val	Val	Glu	Val	Ala	His	Leu	Glu	Glu	Lys	Gln	Gly	Val	Ser	Lys	
		-55					-50					-45				
AGA	CAT	GTT	AGG	ATA	AGC	AGG	TCT	TTG	CAC	CAA	GAT	GAA	CAC	AGC	TGG	1126
Arg	His	Val	Arg	Ile	Ser	Arg	Ser	Leu	His	Gln	Asp	Glu	His	Ser	Trp	
	-40					-35					-30					
TCA	CAG	ATA	AGG	CCA	TTG	CTA	GTA	ACT	TTT	GGC	CAT	GAT	GGA	AAA	GGG	1174
Ser	Gln	Ile	Arg	Pro	Leu	Leu	Val	Thr	Phe	Gly	His	Asp	Gly	Lys	Gly	
-25					-20					-15					-10	
CAT	CCT	CTC	CAC	AAA	AGA	GAA	AAA	CGT	CAA	GCC	AAA	CAC	AAA	CAG	CGG	1222
His	Pro	Leu	His	Lys	Arg	Glu	Lys	Arg	Gln	Ala	Lys	His	Lys	Gln	Arg	
				-5					1				5			
AAA	CGC	CTT	AAG	TCC	AGC	TGT	AAG	AGA	CAC	CCT	TTG	TAC	GTG	GAC	TTC	1270
Lys	Arg	Leu	Lys	Ser	Ser	Cys	Lys	Arg	His	Pro	Leu	Tyr	Val	Asp	Phe	
		10					15					20				
AGT	GAC	GTG	GGG	TGG	AAT	GAC	TGG	ATT	GTG	GCT	CCC	CCG	GGG	TAT	CAC	1318
Ser	Asp	Val	Gly	Trp	Asn	Asp	Trp	Ile	Val	Ala	Pro	Pro	Gly	Tyr	His	
	25					30					35					
GCC	TTT	TAC	TGC	CAC	GGA	GAA	TGC	CCT	TTT	CCT	CTG	GCT	GAT	CAT	CTG	1366

Ala	Phe	Tyr	Cys	His	Gly	Leu	Cys	Pro	Phe	Pro	Leu	Ala	Asp	His	Leu	
40					45					50					55	
TAC	TCC	ACT	AAT	CAT	GCC	ATT	GTT	CAG	ACG	TTG	GTC	AAC	TCT	GTT	AAC	1414
Asn	Ser	Thr	Asn	His	Ala	Ile	Val	Gln	Thr	Leu	Val	Asn	Ser	Val	Asn	
			60					65						70		
TCT	AAG	ATT	CCT	AAG	GCA	TGC	TGT	GTC	CCG	ACA	GAA	CTC	AGT	GCT	ATC	1462
Ser	Lys	Ile	Pro	Lys	Ala	Cys	Cys	Val	Pro	Thr	Glu	Leu	Ser	Ala	Ile	
			75					80						85		
TCG	ATG	CTG	TAC	CTT	GAC	GAG	AAT	GAA	AAG	GTT	GTA	TTA	AAG	AAC	TAT	1510
Ser	Met	Leu	Tyr	Leu	Asp	Glu	Asn	Glu	Lys	Val	Val	Leu	Lys	Asn	Tyr	
	90						95					100				
TAG	GAC	ATG	GTT	GTG	GAG	GGT	TGT	GGG	TGT	CGC	TAGTACAGCA	AAATTAATA				1563
Gln	Asp	Met	Val	Val	Glu	Gly	Cys	Gly	Cys	Arg						
	105					110					115					
TATAAATATA	TATATATATA	TATATTTTAG	AAAAAAGAAA	AAAA												1607

2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 396 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Val	Ala	Gly	Thr	Arg	Cys	Leu	Leu	Ala	Leu	Leu	Leu	Pro	Gln	Val	
-282		-280					-275						-270			
Leu	Leu	Gly	Gly	Ala	Ala	Gly	Leu	Val	Pro	Glu	Leu	Gly	Arg	Arg	Lys	
-265						-260						-255				
Phe	Ala	Ala	Ala	Ser	Ser	Gly	Arg	Pro	Ser	Ser	Gln	Pro	Ser	Asp	Glu	
250				-245						-240					-235	
Val	Leu	Ser	Glu	Phe	Glu	Leu	Arg	Leu	Leu	Ser	Met	Phe	Gly	Leu	Lys	
			-230						-225					-220		
Gln	Arg	Pro	Thr	Pro	Ser	Arg	Asp	Ala	Val	Val	Pro	Pro	Tyr	Met	Leu	
			-215					-210						-205		
Asp	Leu	Tyr	Arg	Arg	His	Ser	Gly	Gln	Pro	Gly	Ser	Pro	Ala	Pro	Asp	
	-200						-195						-190			
His	Arg	Leu	Glu	Arg	Ala	Ala	Ser	Arg	Ala	Asn	Thr	Val	Arg	Ser	Phe	
-185					-180							-175				
His	His	Glu	Glu	Ser	Leu	Glu	Glu	Leu	Pro	Glu	Thr	Ser	Gly	Lys	Thr	
-170				-165						-160					-155	
Thr	Arg	Arg	Phe	Phe	Phe	Asn	Leu	Ser	Ser	Ile	Pro	Thr	Glu	Glu	Phe	
			-150						-145						-140	

Ile Thr Ser Ala Glu Leu Val Phe Arg Glu Gln Met Gln Asp Ala
 -135 -130 -125
 Leu Gly Asn Asn Ser Ser Phe His His Arg Ile Asn Ile Tyr Glu Ile
 -120 -115 -110
 Ile Lys Pro Ala Thr Ala Asn Ser Lys Phe Pro Val Thr Arg Leu Leu
 -105 -100 -95
 Asp Thr Arg Leu Val Asn Gln Asn Ala Ser Arg Trp Glu Ser Phe Asp
 -90 -85 -80 -75
 Val Thr Pro Ala Val Met Arg Trp Thr Ala Gln Gly His Ala Asn His
 -70 -65 -60
 Gly Phe Val Val Glu Val Ala His Leu Glu Glu Lys Gln Gly Val Ser
 -55 -50 -45
 Lys Arg His Val Arg Ile Ser Arg Ser Leu His Gln Asp Glu His Ser
 -40 -35 -30
 Trp Ser Gln Ile Arg Pro Leu Leu Val Thr Phe Gly His Asp Gly Lys
 -25 -20 -15
 Gly His Pro Leu His Lys Arg Glu Lys Arg Gln Ala Lys His Lys Gln
 -10 -5 1 5
 Arg Lys Arg Leu Lys Ser Ser Cys Lys Arg His Pro Leu Tyr Val Asp
 10 15 20
 Phe Ser Asp Val Gly Trp Asn Asp Trp Ile Val Ala Pro Pro Gly Tyr
 25 30 35
 His Ala Phe Tyr Cys His Gly Glu Cys Pro Phe Pro Leu Ala Asp His
 40 45 50
 Leu Asn Ser Thr Asn His Ala Ile Val Gln Thr Leu Val Asn Ser Val
 55 60 65 70
 Asn Ser Lys Ile Pro Lys Ala Cys Cys Val Pro Thr Glu Leu Ser Ala
 75 80 85
 Ile Ser Met Leu Tyr Leu Asp Glu Asn Glu Lys Val Val Leu Lys Asn
 90 95 100
 Tyr Gln Asp Met Val Val Glu Gly Cys Gly Cys Arg
 105 110

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1954 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo Sapiens
- (G) CELL TYPE: Osteosarcoma Cell Line
- (H) CELL LINE: U-2OS

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: U2OS cDNA in Lambda gt10
- (B) CLONE: Lambda U2OS-3

(viii) POSITION IN GENOME:

- (C) UNITS: bp

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 403..1629

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1279..1626

(ix) FEATURE:

- (A) NAME/KEY: mRNA
- (B) LOCATION: 9..1934

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CTCTAGAGGG CAGAGGAGGA GGGAGGGAGG GAAGGAGCGC GGAGCCCGGC CCGGAAGCTA 60
GGTGAGTGTG GCATCCGAGC TGAGGGACGC GAGCCTGAGA CGCCGCTGCT GCTCCGGCTG 120
AGTATCTAGC TTGTCTCCCC GATGGGATTC CCGTCCAAGC TATCTCGAGC CTGCAGCGCC 180
ACAGTCCCCG GCCCTCGCCC AGGTTCACTG CAACCGTTCA GAGGTCCCCA GGAGCTGCTG 240
CTGGCGAGCC CGCTACTGCA GGGACCTATG GAGCCATTCC GTAGTGCCAT CCCGAGCAAC 300
GCACTGCTGC AGCTTCCCTG AGCCTTTCCA GCAAGTTTGT TCAAGATTGG CTGTCAAGAA 360
TCATGGACTG TTATTATATG CCTTGTTTTT TGTCAAGACA CC ATG ATT CCT GGT 414
Met Ile Pro Gly
-292 -290
AAC CGA ATG CTG ATG GTC GTT TTA TTA TGC CAA GTC CTG CTA GGA GGC 462
Asn Arg Met Leu Met Val Val Leu Leu Cys Gln Val Leu Leu Gly Gly
-285 -280 -275
GCG AGC CAT GCT AGT TTG ATA CCT GAG ACG GGG AAG AAA AAA GTC GCC 510
Ala Ser His Ala Ser Leu Ile Pro Glu Thr Gly Lys Lys Lys Val Ala
-270 -265 -260
GAG ATT CAG GGC CAC GCG GGA GGA CGC CGC TCA GGG CAG AGC CAT GAG 558
Glu Ile Gln Gly His Ala Gly Gly Arg Arg Ser Gly Gln Ser His Glu
-255 -250 -245
CTC CTG CGG GAC TTC GAG GCG ACA CTT CTG CAG ATG TTT GGG CTG CGC 606
Leu Leu Arg Asp Phe Glu Ala Thr Leu Leu Gln Met Phe Gly Leu Arg

Gln Ser His Glu Leu Leu Arg Asp Phe Glu Ala Thr Leu Leu Gln Met
 -240 -235 -230

Phe Gly Leu Arg Arg Arg Pro Gln Pro Ser Lys Ser Ala Val Ile Pro
 -225 -220 -215

Asp Tyr Met Arg Asp Leu Tyr Arg Leu Gln Ser Gly Glu Glu Glu Glu
 -210 -205 -200

Glu Gln Ile His Ser Thr Gly Leu Glu Tyr Pro Glu Arg Pro Ala Ser
 -195 -190 -185

Arg Ala Asn Thr Val Arg Ser Phe His His Glu Glu His Leu Glu Asn
 -180 -175 -170 -165

Ile Pro Gly Thr Ser Glu Asn Ser Ala Phe Arg Phe Leu Phe Asn Leu
 -160 -155 -150

Ser Ser Ile Pro Glu Asn Glu Val Ile Ser Ser Ala Glu Leu Arg Leu
 -145 -140 -135

Phe Arg Glu Gln Val Asp Gln Gly Pro Asp Trp Glu Arg Gly Phe His
 -130 -125 -120

Arg Ile Asn Ile Tyr Glu Val Met Lys Pro Pro Ala Glu Val Val Pro
 -115 -110 -105

Gly His Leu Ile Thr Arg Leu Leu Asp Thr Arg Leu Val His His Asn
 -100 -95 -90 -85

Val Thr Arg Trp Glu Thr Phe Asp Val Ser Pro Ala Val Leu Arg Trp
 -80 -75 -70

Thr Arg Glu Lys Gln Pro Asn Tyr Gly Leu Ala Ile Glu Val Thr His
 -65 -60 -55

Leu His Gln Thr Arg Thr His Gln Gly Gln His Val Arg Ile Ser Arg
 -50 -45 -40

Ser Leu Pro Gln Gly Ser Gly Asn Trp Ala Gln Leu Arg Pro Leu Leu
 -35 -30 -25

Val Thr Phe Gly His Asp Gly Arg Gly His Ala Leu Thr Arg Arg Arg
 -20 -15 -10 -5

Arg Ala Lys Arg Ser Pro Lys His His Ser Gln Arg Ala Arg Lys Lys
 1 5 10

Asn Lys Asn Cys Arg Arg His Ser Leu Tyr Val Asp Phe Ser Asp Val
 15 20 25

Gly Trp Asn Asp Trp Ile Val Ala Pro Pro Gly Tyr Gln Ala Phe Tyr
 30 35 40

Cys His Gly Asp Cys Pro Phe Pro Leu Ala Asp His Leu Asn Ser Thr
 45 50 55 60

Asn His Ala Ile Val Gln Thr Leu Val Asn Ser Val Asn Ser Ser Ile
 65 70 75

